S7 Fig. The whole-genome distribution of TEs annotated using TIRs derived from TIR Learner.
Density plots generated using Circos [1] for the distribution of the annotated TEs in *Zea mays* (**A**) and
Oryza sativa (**B**) genomes. TE superfamilies are coloured and separated by track, ordered by their
relative abundance in the genome. The distribution of genes (in grey) is plotted for comparison. The
outer track displays genomic positions while the horizontal axis refers to TE frequency.

Reference:
1. Krzywinski MI, Schein JE, Birol I, Connors J, Gascoyne R, Horsman D, et al. Circos: An information
   aesthetic for comparative genomics. Genome Res. 2009 [cited 16 Dec 2021].
   doi:10.1101/gr.092759.109